

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE CLAIMS:

Please amend claims 17 as follows:

17. A physical platform comprising an array of nucleic acid polymers immobilized at [a] predetermined positions on a solid support:

wherein the array is comprised of at least two different isolated nucleic acid polymers which are each specific for a different gene associated with lipid metabolism, synthesis, or action; and

genomic DNA derived from a patient tissue sample [that is further comprised of a label and] [that contacts] that is hybridized to the array [under conditions wherein hybridization of the genomic DNA and the immobilized nucleic acid polymers are determined by] and is detectable by a [the] label at the predetermined positions of [at] the at least two isolated nucleic acid polymers, wherein detection of the label at the predetermined positions indicates a difference in copy number of at least two different genes associated with lipid metabolism, synthesis or action.

RESPONSE

In response to the previous action, Applicant amended the claims to define the invention by reciting structure for the detection of the copy number of a plurality of genes in the genomic DNA of a patient sample, rather than the detection of gene expression. As the Examiner has recognized, one aspect of the invention is directed to detection of the copy number of a gene represented in the entire genome of a patient and that this approach is not the same as measuring gene expression. The claim amendment submitted previously and those detailed above, are submitted to structurally distinguish the prior art arrays that merely analyze gene expression in a sample.

Accordingly, the DeRisi reference is a conventional array for multiplex analysis of gene expression. The labelled (YOYO) DNA is printed on the array as part of the device. (See legend to FIG. 1). In DeRisi, there is no genomic DNA from a patient sample hybridized and labelled at the functional components of the array, such that copy number information in the sample is provided. In fact, there is no reason for such a species to exist in DeRisi because it would not facilitate DeRisi's use of labelled mRNA to detect gene expression. Applicants appreciate the Examiner's point regarding the inability of an intended use to distinguish a reference that is not structurally distinguished from the prior art. For this reason, the previous amendment specified that the array was combined into a platform with patient genomic DNA. The structural difference is provided by the use of patient genomic DNA in combination with an array whose member nucleic acid polymers are directed to measurement of lipid-related genes and a labelled hybridization event that yields information about copy number of the genes selected for the array. This structure distinguishes conventional arrays when labelled mRNA, derived from patient cell sample, etc., are hybridized with

cDNA arrays to detect the underlying expression occurring in the sample. Essentially, the claimed structure combines labelled genomic patient DNA hybridized to an isolated nucleic acid polymer as a member of a predetermined array, rationally associated with lipid metabolism, synthesis, or action, and is not found in the cited references. Regarding the § 103 rejection over Chee (USP 5,840,484) and/or any of Lockhart et al., Gao et al., Fukushima et al., Goetzl et al., Haapamski et al., Gibbs et al., none of the claims are rendered obvious by any combination because a prima facie case under § 103 does not exist because none of these references provide the element of a labelled hybridization even between genomic DNA and a member of the array. Absent a prima facie case, one cannot draw the conclusion that the invention as a whole would have been obvious to one of ordinary skill in the art at the time the invention was made. M.P.E.P. § 2142.

Thus, Applicant's previous amendments are not directed to intended use, but rather are to specify, structurally, that the invention is not a generic array structure for the analysis of gene expression, but is a specific combination of elements, both a rationally organized array element and a genomic DNA sample for determination of copy number rather than gene expression.

Applicants recognize the Examiner's rationale regarding the selection of genes for expression analysis and the motivation to create arrays for this purpose. However, this motivation does not yield a structure where genomic DNA from a patient sample hybridizes in the array as claimed. Applicants submit that this difference is fundamentally structural – not a question of intended use or method of manufacture. For this reason, none of the secondary references (in addition to DeRisi) cure the deficiencies of DeRisi that derive from DeRisi's stated purpose of gene expression analysis.

The deficiencies in the secondary references were detailed in the previous response.

Applicant simply notes that none of the references disclose a hybridization complex of labelled

genomic DNA in a nationally selected array such that chromosomal abnormalities in genes related to lipid metabolism synthesis or action are detected.

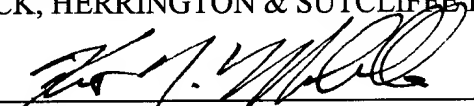
None of the cited references suggest the approach of measuring copy number of the selected genes in a specific biological network. A rejection under §103(a) cannot be made absent a particular finding that justifies a conclusion that the skilled artisan would have had the motivation to combine or modify the cited references to reach the invention claimed.

For all of these reasons, Applicant submits that the pending claims are not rendered obvious by any combination of the cited references, and are in condition for allowance.

Respectfully submitted,

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